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10/817,244	04/03/2004	Zohar Yakhini	10020503-2	3028

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EXAMINER	
NEGIN, RUSSELL SCOTT	
ART UNIT	**PAPER NUMBER**
1631	

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
3 MONTHS	04/18/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

Office Action Summary	Application No.	Applicant(s)	
	10/817,244	YAKHINI ET AL.	
	Examiner	Art Unit	
	Russell S. Negin	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *17 October 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-79* is/are pending in the application.

4a) Of the above claim(s) *57-79* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-33,55 and 56* is/are rejected.

7)☒ Claim(s) *20 and 34-55* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *10/17/06; 4/3/2004*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

Applicant's election with traverse of Group I, species CGH in the reply filed on 17 October 2006 is acknowledged. The traversal is on the ground(s) that there is not undue burden to search all of the groups in this application. This is not found persuasive because Groups II and III have features resulting in extra necessary search and consideration. The reordering of rows in maps in Group II and the system for visualizing chromosome maps in Group III require additional search considerations.

The requirement is still deemed proper and is therefore made FINAL.

Claims 57-79 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected Group, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on 17 October 2006.

Applicant additionally argued that the species election in claim 24 is misunderstood. Applicant argued that there is not unreasonable search burden and therefore the species election should be withdrawn. This argument is found to be persuasive, and the species election requirement for claim 24 is withdrawn.

Specification

The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

Specifically, line 8 of page 2, line 15 of page 4, and line 6 of page 16 have embedded hyperlinks.

Claim Objections

Claims 20 and 55 are objected to because of the following informalities:

Claim 20 is a marked up claim. It is assumed that the phrase "values assessed" is absent from the instant claim.

Claim 55 has the term "claim1" as a single term.

Appropriate correction is required.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-3, 7, 12-15 and 27-28 are rejected under 35 U.S.C. 102(b) as being anticipated by Ben-Dor et al. [Genome Research, 2000, volume 10, pages 365-378]

Claims 1-3, 7, 12-15 and 27-28 state:

1. A method for overlaying gene- or protein-related data on chromosome maps, said method comprising the steps of: importing arbitrary gene- or protein-related data having identifiers for determining genetic loci of genes to which said arbitrary gene-related data are associated; reading the identifiers; matching the identifiers with predefined identifiers on at least one of the chromosome maps; and displaying the arbitrary gene- or protein related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene- or protein-related data are located, wherein said importing, reading, matching and displaying are all automated

steps.

2. The method of claim 1, further comprising interactive selection by a user of at least one data type to be displayed during said displaying.

3. The method of claim 1, further comprising spatially grouping said gene- or protein-related data to correspond to spatial groupings of said associated genes on said at least one chromosome map.

7. The method of claim 1, wherein said at least one chromosome map comprises a plurality of chromosome maps, said method further comprising maintaining focus and context of at least a portion of the display of said chromosome maps and gene- or protein-related data.

12. The method of claim 1, further comprising accessing an external source of information relative to the data displayed, matching at least one of said identifiers with specific information in said external source; and displaying said specific information relative to said gene- or protein-related data associated with said at least one identifier.

13. The method of claim 1, wherein said identifiers of said arbitrary gene- or protein-related data are selected from published gene identifiers and symbols.

14. The method of claim 13, wherein said published gene identifiers and symbols are selected from at least one of GenBank accession numbers, RefSeq accession numbers, UniGene Cluster ID's, UniGene ID's, official standard gene names, LocusLink ID, SwissProt ID's, and Protein Information Resource (PIR) ID's.

15. The method of claim 1, wherein said matching comprises providing a relational database which stores a set of cross-referenced tables for matching said identifiers with said predefined identifiers, and as the identifiers are read, they are matched with said predefined identifiers in the cross-referenced tables through standard database queries.

27. The method of claim 1, wherein said arbitrary gene- or protein- related data is imported from a plurality of experiments.

28. The method of claim 27, wherein said arbitrary gene- or protein- related data is displayed with regard to each of the plurality of experiments on a single display.

The article of Ben-Dor et al., entitled, "RHO-Radiation Hybrid Ordering" states in its abstract:

> Radiation hybrid (RH) mapping is a somatic cell technique that is used for ordering markers along a chromosome and estimating the physical distances between them. With the advent of this mapping technique, analyzing the experimental data is becoming a challenging and demanding computational task. In this paper we present the software package RHO (radiation hybrid ordering). This package implements a number of heuristics to order genomic markers along a chromosome, given as input the results of an RH experiment.

The gene data is imported from the Whitehead Institute (the external source) as stated in the lines bridging columns 1 and 2 of page 368 of Ben-Dor et al.:

> The RH data used to construct the maps was downloaded from the Whitehead Institute for Biomedical Research.

Identifiers are listed in Table 4 of page 371 of Ben-Dor et al. and the matching process is described in lines 7-23 of column 2 of page 371 to lines 1-5 of column 1 of page 372:

> Different maps of the same chromosome give rise to different estimates of its total physical length. Shorter maps are generally viewed as more desirable ones. This transformation of probabilities to distances is implemented in RHMAPPER. Using this implementation, we conclude that the total physical length of chromosome 2 in our map is 3.88% shorter that in the WI framework map... The detailed differences between the two maps are depicted graphically in Figure 6. These map portions are drawn to scale.

Consequently, Figure 6 of Ben-Dor et al. maps the chromosome identifiers between the chromosome 2 map and the WI framework map. The data in Figure 6 of Ben-Dor et al. are spatially grouped on the chromosome map. There is a plurality of chromosome maps illustrated in Figure 6 of Ben-Dor et al.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

35 U.S.C. 103 Rejection #1:

Claims 1, 16, 18, 20-26, 29-33, and 55-56 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. in view of Stanyon et al. [Cytogenetics and Cell Genetics, volume 84, 1999, pages 150-155].

Claims 16, 18, 20-26, 29-33, and 55-56 state:

16. The method of claim 1, wherein said arbitrary gene- or protein-related data comprises an expression matrix.

18. The method of claim 1, wherein said arbitrary gene- or protein-related data comprises a matrix of at least one microarray of gene expression data, wherein each row of the matrix is associated with a particular gene, and wherein said matching comprises reordering and spatial grouping of the rows based on matching the identifiers to the predefined identifiers.

20. The method of claim 1, further comprising statistically assessing co-location values and displaying assessed co-location statistical significance along side said arbitrary gene-related data.

21. The method of claim 1, further comprising the steps of: selecting additional information characterizing said arbitrary gene- or protein-related data; and displaying

said additional information along side of said display of the arbitrary gene- or protein-related data and positioned relative to the respective locations on the chromosome map of the respective genes characterized by said arbitrary gene- or protein-related data.

22. The method of claim 21, wherein said additional information comprises annotations.

23. The method of claim 22, wherein said annotations comprise gene ontology annotations.

24. The method of claim 21, wherein said additional information is selected from the group consisting of CGH data, protein levels, relevance scores and relevance densities.

25. The method of claim 22, wherein said arbitrary gene- or protein-related data is displayed in matrix format and said additional information is displayed in at least one additional matrix.

26. The method of claim 21, wherein said arbitrary gene- or protein-related data is displayed in scatter plot format.

29. The method of claim 21, wherein said additional information includes at least one of annotations, cellular localization of the genetic material, cluster data, and statistical data.

30. The method of claim 18, further comprising calculating row vectors of the values in the rows of the matrix; using an auxiliary process to obtain cluster data for said row vectors; and displaying said cluster data along side said display of said arbitrary gene- or protein-related data.

31. The method of claim 30, wherein said matrix comprises a heat map, and wherein said cluster data and said arbitrary gene- or protein-related data are displayed with color coding.

32. The method of claim 30, wherein said cluster data is displayed in a single column adjacent each matrix of gene- or protein-related data.

33. The method of claim 30, wherein said cluster data is displayed in a multi-column matrix adjacent each matrix of gene- or protein-related data, respectively.

55. The method of claim 1, further comprising the steps of: selecting additional information related to one or more genes characterized by said arbitrary gene- or protein-related data; and displaying said additional information along side of said display of the arbitrary gene- or protein-related data and positioned relative to the respective locations on the chromosome map of the respective genes characterized by said arbitrary gene- or protein-related data.

56. The method of claim 55, wherein said additional information comprise at least one of polymorphism measurements, annotations, transcription factor binding sites, RNA expression values, allele information, alternative exon splicing data, mapping of CGH gene amplification/deletions, and protein abundance.

The article of Ben-Dor et al., entitled, "RHO-Radiation Hybrid Ordering" states in its abstract:

> Radiation hybrid (RH) mapping is a somatic cell technique that is used for ordering markers along a chromosome and estimating the physical distances between them. With the advent of this mapping technique, analyzing the experimental data is becoming a challenging and demanding computational task. In this paper we present the software package RHO (radiation hybrid ordering). This package implements a number of heuristics to order genomic markers along a chromosome, given as input the results of an RH experiment.

The gene data is imported from the Whitehead Institute as stated in the lines bridging columns 1 and 2 of page 368 of Ben-Dor et al.:

> The RH data used to construct the maps was downloaded from the Whitehead Institute for Biomedical Research.

Identifiers are listed in Table 4 of page 371 of Ben-Dor et al. and the matching process is described in lines 7-23 of column 2 of page 371 to lines 1-5 of column 1 of page 372:

> Different maps of the same chromosome give rise to different estimates of its total physical length. Shorter maps are generally viewed as more desirable ones. This transformation of probabilities to distances is implemented in RHMAPPER. Using this implementation, we conclude that the total physical length of chromosome 2 in our map is 3.88% shorter that in the WI framework map... The detailed differences between the two maps are depicted graphically in Figure 6. These map portions are drawn to scale.

Consequently, Figure 6 of Ben-Dor et al. maps the chromosome identifiers between the chromosome 2 map and the WI framework map. The data in Figure 6 of Ben-Dor et al. are spatially grouped on the chromosome map. There is a plurality of chromosome maps illustrated in Figure 6 of Ben-Dor et al.

However, Ben-Dor et al. does not show expression matrices, statistical significance, adding additional information to the chromosome map, annotations, scores, or statistical analyses of the matrices.

The article of Stanyon et al., entitled, "Reciprocal chromosome painting shown that genomic rearrangement between rat and mouse proceeds ten times faster than between humans and cats," states in the first sentence of the abstract:

> Reciprocal chromosome painting between mouse and rat using complete chromosome probe sets of both species permitted us to assign chromosomal homology between these rodents.

The purpose of the study is explained on page 151, column 1, lines 7-10, which state:

> Reciprocal chromosome painting between rat and mouse allows a transfer of gene mapping data from mouse to rat and vice versa, thus aiding in both disease and genetic trait analyses.

The annotated chromosome maps of the rat and mouse are shown in Figures 3 and 4 of page 152 of Stanyon et al. The numbers annotations are used for the comparison of rat to mouse genetic homologies.

A matrix is shown which compares the expression data between mouse and rat on page 153 of Stanyon et al. in which similarities are scored by coloring the tiles in the matrices. The statistics of each row and column of the matrix are enumerated in numbers that border each row and column of the matrix. These statistics represent the percent agreement between FISH and gene mapping. The matrix is color coded according the expression data and the clusters of data are evaluated in the numbers bordering each column and row on the matrix.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the radiation hybrid ordering method of Ben-Dor et al. in

view of the homology study of Stanyon et al. because while Ben-Dor et al. examines differences in databases and labeling techniques through chromosome mapping and matching, Stanyon et al. uses these techniques of mapping and matching to determining similarities between the genomes of different species to aid in disease and genetic trait analyses.

35 U.S.C. 103 Rejection #2:

Claims 1 and 4-11 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. in view of Koleszar et al. [US Patent 6,519,583].

Claims 4-6 and 8-11 state:

4. The method of claim 1, further comprising compressing said gene- or protein-related data when required to display said gene- or protein-related data in an area in which all of the gene- or protein-related data cannot be discretely displayed.

5. The method of claim 1, further comprising zooming at least one of said gene- or protein-related data and said at least one chromosome map to display an enlarged view of additional detail relevant to a zoomed area.

6. The method of claim 1, further comprising querying and cutting information on the display that a user is not interested in viewing.

8. The method of claim 7, further comprising displaying a high level view of all of said chromosome maps and gene- or protein-related data, a mid-level view displaying a magnified view of a selected portion of said high level view, and a detailed view displaying expanded, detailed information characterizing a selected portion of said mid-level view.

9. The method of claim 8, wherein said high-level view, mid-level view and detailed view are all interlinked so that changing one view automatically changes the other two views in the same way, substantially simultaneously.

10. The method of claim 1, further comprising displaying tooltips to display additional details relative to a selected portion of the display.

11. The method of claim 1, further comprising displaying popup dialogs to display additional details relative to a selected portion of the display.

The article of Ben-Dor et al., entitled, "RHO-Radiation Hybrid Ordering" states in its abstract:

> Radiation hybrid (RH) mapping is a somatic cell technique that is used for ordering markers along a chromosome and estimating the physical distances between them. With the advent of this mapping technique, analyzing the experimental data is becoming a challenging and demanding computational task. In this paper we present the software package RHO (radiation hybrid ordering). This package implements a number of heuristics to order genomic markers along a chromosome, given as input the results of an RH experiment.

The gene data is imported from the Whitehead Institute as stated in the lines bridging columns 1 and 2 of page 368 of Ben-Dor et al.:

> The RH data used to construct the maps was downloaded from the Whitehead Institute for Biomedical Research.

Identifiers are listed in Table 4 of page 371 of Ben-Dor et al. and the matching process is described in lines 7-23 of column 2 of page 371 to lines 1-5 of column 1 of page 372:

> Different maps of the same chromosome give rise to different estimates of its total physical length. Shorter maps are generally viewed as more desirable ones. This transformation of probabilities to distances is implemented in RHMAPPER. Using this implementation, we conclude that the total physical length of chromosome 2 in our map is 3.88% shorter that in the WI framework map... The detailed differences between the two maps are depicted graphically in Figure 6. These map portions are drawn to scale.

Consequently, Figure 6 of Ben-Dor et al. maps the chromosome identifiers between the chromosome 2 map and the WI framework map. The data in Figure 6 of Ben-Dor et al. are spatially grouped on the chromosome map. There is a plurality of chromosome maps illustrated in Figure 6 of Ben-Dor et al.

Ben-Dor et al. fails to teach the use of a display to analyze the data (i.e. zooming in to display the additional data as claimed in the instant set of claims).

The invention of Koleszar et al., entitled, "Graphical viewer for biomolecular sequence data," states in the abstract:

> Disclosed are methods, media and systems for graphically displaying computer-based biomolecular sequence information. Generally, biomolecular sequence information may be graphically depicted in a variety of different forms in accordance with the present invention. The sequence information may be composed of nucleotide or amino acid sequence information or both. The graphical depictions may be in several different formats providing different information relating to the sequences, and may be displayed in one or more screens of a computer user interface.

Figure 4A has the ability to zoom in on regions or zooming out and compressing regions of the genomic sequence of interest as is illustrated on the toolbar of the schematic with pop-up buttons to control the viewing of the features.

The purpose of Koleszar et al. in explained in column 2, lines 5-9, which states:

> Accordingly, the development if a display tool which allows a user to clearly and effectively display gene loci information for a given organism or organisms and.or other biomolecular sequences in desirable.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify Ben-Dor et al. by use of Koleszar et al., because Koleszar et al. has the advantage of displaying the genomic data of Ben-Dor et al. in a more convenient and user-friendly format.

35 U.S.C. 103 Rejection #3:

Claims 1 and 16-19 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. in view of Singer et al. [US Patent 5,866,331].

Claims 16-19 state:

16. The method of claim 1, wherein said arbitrary gene- or protein-related data comprises an expression matrix.

17. The method of claim 16, wherein said arbitrary gene- or protein-related data comprises a plurality of expression matrices.

18. The method of claim 1, wherein said arbitrary gene- or protein-related data comprises a matrix of at least one microarray of gene expression data, wherein each row of the matrix is associated with a particular gene, and wherein said matching comprises reordering and spatial grouping of the rows based on matching the identifiers to the predefined identifiers.

19. The method of claim 18, wherein a visualization of the matrix resultant from said displaying comprises a heat map.

The article of Ben-Dor et al., entitled, "RHO-Radiation Hybrid Ordering" states in its abstract:

> Radiation hybrid (RH) mapping is a somatic cell technique that is used for ordering markers along a chromosome and estimating the physical distances between them. With the advent of this mapping technique, analyzing the experimental data is becoming a challenging and demanding computational task. In this paper we present the software package RHO (radiation hybrid ordering). This package implements a number of heuristics to order genomic markers along a chromosome, given as input the results of an RH experiment.

The gene data is imported from the Whitehead Institute as stated in the lines bridging columns 1 and 2 of page 368 of Ben-Dor et al.:

> The RH data used to construct the maps was downloaded from the Whitehead Institute for Biomedical Research.

Identifiers are listed in Table 4 of page 371 of Ben-Dor et al. and the matching process is described in lines 7-23 of column 2 of page 371 to lines 1-5 of column 1 of page 372:

> Different maps of the same chromosome give rise to different estimates of its total physical length. Shorter maps are generally viewed as more desirable ones. This transformation of probabilities to distances is implemented in RHMAPPER. Using this implementation, we conclude that the total physical length of chromosome 2 in our map is 3.88% shorter that in the WI framework map... The detailed differences between the two maps are depicted graphically in Figure 6. These map portions are drawn to scale.

Consequently, Figure 6 of Ben-Dor et al. maps the chromosome identifiers between the chromosome 2 map and the WI framework map. The data in Figure 6 of Ben-Dor et al. are spatially grouped on the chromosome map. There is a plurality of chromosome maps illustrated in Figure 6 of Ben-Dor et al.

Ben-Dor et al. fails to teach heat maps on a plurality of matrices.

The invention of Singer et al., entitled, "Single molecule detection by in situ hybridization," states that its purpose is to use cell microscopy, biology, and digital imaging to better detect shorter target sequences. As is stated in column 4, lines 49-51, "As few as five fluorochromes on a single probe provide a sufficiently strong signal for a detection of that single probe."

Figures 2A and 2B illustrate a plurality of heat maps used to detect hybridizations to nucleotide probes.

It would have been obvious at the time of the instant invention for someone of ordinary skill in the art to modify the radiation hybridization ordering study of Ben-Dor et al. by use of the heat maps shown in Singer et al. because while Ben-Dor et al. generate the generic maps used to assess chromosomal topology, Singer et al. uses advanced mapping techniques to better detect hybridization to short target sequences.

Allowable Subject Matter

Claims 34-54 are objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

Conclusion

No claim is allowed.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the central PTO Fax Center. The faxing of such pages must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993)(See 37 CFR § 1.6(d)). The Central PTO Fax Center Number is (571) 273-8300.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Russell Negin, Ph.D., whose telephone number is (571) 272-1083. The examiner can normally be reached on Monday-Friday from 7am to 4pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's Supervisor, Ram Shukla, Supervisory Patent Examiner, can be reached at (571) 272-0735.

Information regarding the status of the application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information on the PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

RSN
13 April 2007

4/13/07

13 April 2007

JOHN S. BRUSCA, PH.D
PRIMARY EXAMINER